

Supplementary Materials

Growth rate, transmission mode and virulence in human pathogens

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Fig. S1: The pattern of case fatality rate (%: red circles), infective dose (log: blue circles) and generations per week (log: green circles) across the phylogeny. The size of circles represent phenotypic values.

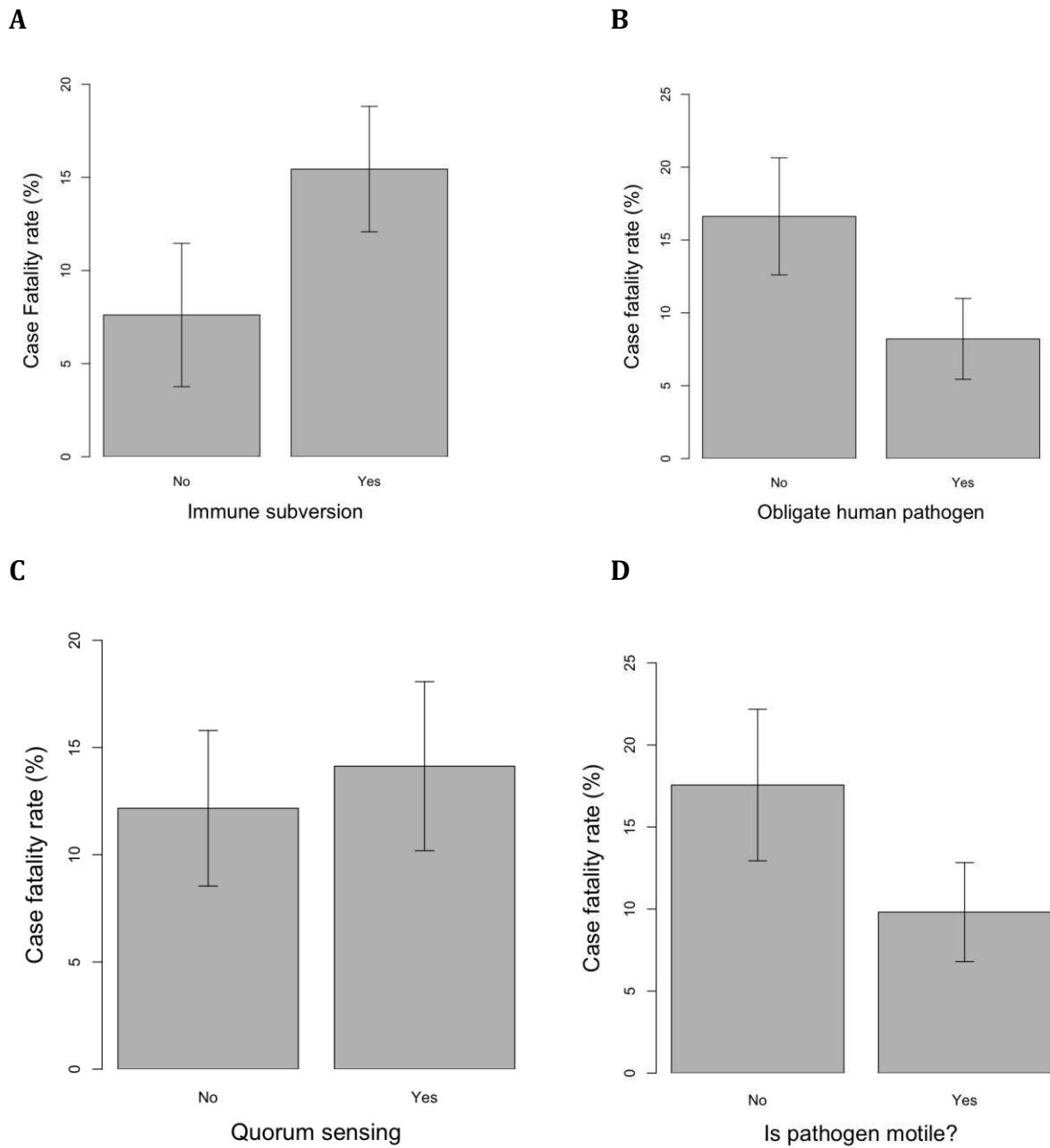


Fig S2. Virulence and parasite life history. The case fatality rate (log number of deaths per 10,000) cases was not correlated with: **(a)** how symptoms of infection affect transmission; **(b)** whether species require a human infection to complete their life cycle (facultative), or not (obligate); **(c)** whether quorum sensing was used to control the production of virulence factors; **(d)** whether species are motile or not (Table S1; S3)

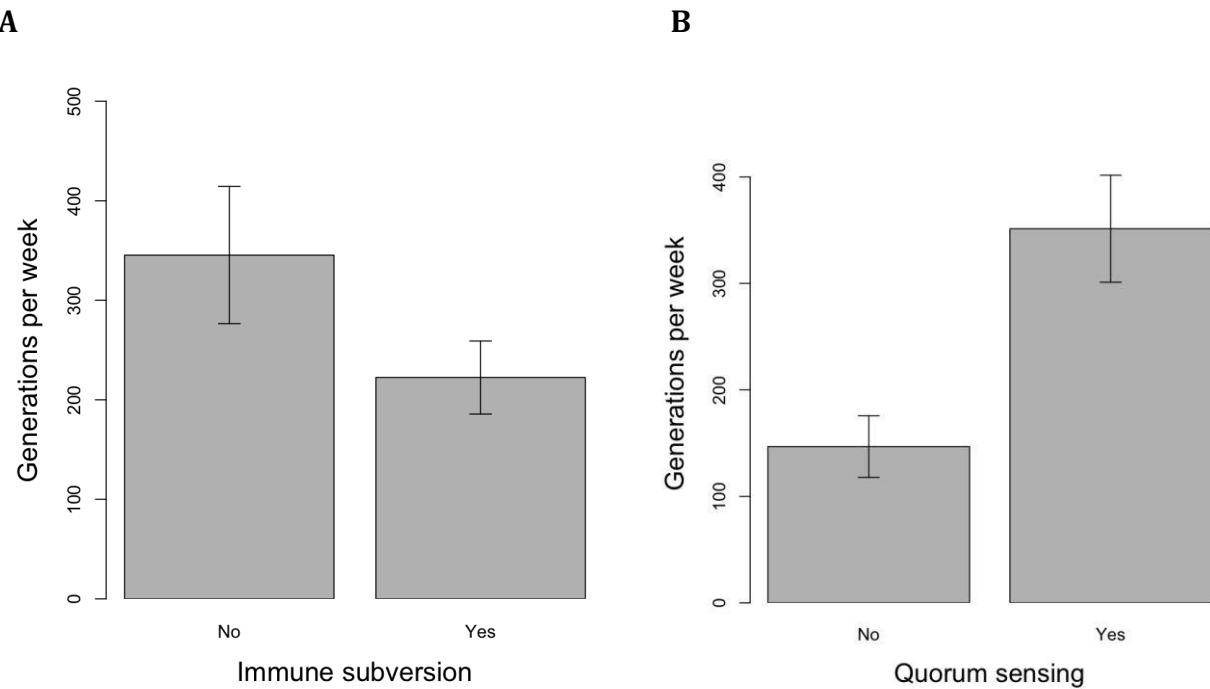


Fig. S3. Growth rates and parasite life history. **(a)** We did not find a significant relationship between immune subversion and generation time (Table S3; S5). **(b)** The generation time of pathogens is significantly lower where quorum sensing was used to control production of virulence factors (Table S3, Table S5).

Table S1. The phylogenetic and residual correlations between case fatality rate (% of cases that result in fatalities: binomial response, logit link function), and the number of generations per week (Poisson response, log link function) across human pathogens estimated using multi-response phylogenetic mixed models. The analysis did not include any other life-history traits.

Response Traits	Random effects	Posterior mode (CI)	Phylo H ² (CI)
Case fatality rate	Phylogenetic variance (V_{a1})	0.02 (0.00, 3.08)	0.14 (0.00, 31.80)
	Residual variance (V_{e1})	7.97 (3.55, 11.60)	
Generation time	Phylogenetic variance (V_{a2})	1.54 (1.03, 2.47)	97.48 (91.39, 99.95)
	Residual variance (V_{e2})	0.03 (0.001, 0.15)	
Correlation			P
Case fatality rate: Generation time	Phylogenetic correlation ($Cov_{a1, a2}/\sqrt{V_{a1} * V_{a2}}$)	-0.99 (-0.99, 0.94)	0.43
	Residual correlation ($Cov_{e1, e2}/\sqrt{V_{e1} * V_{e2}}$)	-0.99 (-0.99, -0.66)	0.009

Table S2. The phylogenetic and residual correlations between case fatality rate (% of cases that result in fatalities: binomial response, logit link function), and the number of generations per week (Poisson response, log link function) across only bacterial human pathogens estimated using multi-response phylogenetic mixed models. The analysis did not include any other life-history traits.

Response Traits	Random effects	Posterior mode (CI)	Phylo H ² (CI)
Case fatality rate	Phylogenetic variance (V_{a1})	0.01 (0.00, 4.78)	0.11 (0.00, 43.35)
	Residual variance (V_{e1})	7.83 (3.68, 14.05)	
Generation time	Phylogenetic variance (V_{a2})	1.59 (0.99, 2.45)	98.32 (92.43, 99.95)
	Residual variance (V_{e2})	0.03 (0.001, 0.13)	
Correlation			P
Case fatality rate: Generation time	Phylogenetic correlation ($Cov_{a1, a2}/\sqrt{V_{a1} * V_{a2}}$)	-0.99 (-0.99, 0.92)	0.30
	Residual correlation ($Cov_{e1, e2}/\sqrt{V_{e1} * V_{e2}}$)	-0.99 (-0.99, -0.39)	0.02

Table S3: The phylogenetic and residual correlations between case fatality rate (% of cases that result in fatalities: binomial response, logit link function), and the number of generations per week (Poisson response, log link function) across human pathogens estimated using multi-response phylogenetic mixed models with life-history traits included as fixed effects.

Fixed effect estimates are on the scale of the link function for each response trait.

Response Trait	Fixed effects	Posterior mode (CI)	pMCMC
Case fatality rate	Immune subversion: No	-3.27 (-5.60, -1.22)	
	Immune subversion: Yes	-2.46 (-4.78, -1.06)	
	Difference	-0.48 (-2.11, 1.11)	0.27
	Infection route: Ingestion	-3.80 (-6.23, -2.07)	
	Infection route: Inhalation	-0.30 (-2.52, 1.56)	
	Infection route: Skin	-1.24 (-3.08, 0.63)	
	Ingestion - inhalation	-3.41 (-5.20, -1.52)	0.001
	Ingestion - skin	-2.67 (-4.76, -1.32)	0.001
	Inhalation - skin	0.29 (-1.43, 2.49)	0.30
	Symptoms: hinder (1)	-1.78 (-4.72, 0.13)	
	Symptoms: no effect (2)	-2.58 (-4.33, -0.13)	
	Symptoms: help (3)	-3.43 (-5.61, -1.88)	
	Difference 1 - 2	-0.09 (-2.24, 2.23)	0.47
	Difference 1 - 3	0.66 (-0.88, 3.36)	0.13
	Difference 2 - 3	1.24 (-0.23, 3.09)	0.06
	Facultative	-2.50 (-4.99, -0.65)	
	Obligate	-3.89 (-5.77, -1.33)	
	Difference	0.67 (-0.93, 2.22)	0.23
	Quorum Sensing: No	-3.43 (-5.08, -0.76)	
	Quorum Sensing: Yes	-3.29 (-5.37, -1.05)	
	Difference	0.14 (-1.34, 1.63)	0.433
	Pathogen motility: No	-3.28 (-5.32, -1.18)	
	Pathogen motility: Yes	-2.98 (-4.46, -0.27)	
	Difference	-0.28 (-2.13, 0.78)	0.21
Generation Time	Immune subversion: No	3.61 (1.96, 4.60)	
	Immune subversion: Yes	3.53 (2.22, 4.65)	
	Difference	-0.24 (-0.63, 0.32)	0.31
	Infection route: Ingestion	3.31 (1.68, 4.27)	
	Infection route: Inhalation	2.71 (1.38, 4.15)	
	Infection route: Skin	2.90 (1.60, 3.99)	
	Ingestion vs inhalation	0.28 (-0.30, 0.89)	0.11

		Posterior mode (CI)	Phylo H ² (CI)
Ingestion vs skin	0.18 (-0.32, 0.91)	0.15	
Inhalation vs skin	0.04 (-0.78, 0.71)	0.48	
Symptoms: hinder (1)	2.90 (1.42, 4.63)		
Symptoms: no effect (2)	3.42 (2.17, 4.40)		
Symptoms: help (3)	2.79 (1.81, 4.05)		
Difference 1 - 2	-0.33 (-1.17, 0.85)	0.38	
Difference 1 - 3	0.20 (-1.05, 0.96)	0.46	
Difference 2 - 3	0.01 (-0.31, 0.70)	0.21	
Facultative	3.67 (1.73, 4.48)		
Obligate	3.47 (1.72, 4.52)		
Difference	0.18 (-0.50, 0.60)	0.36	
Quorum Sensing: No	3.16 (1.93, 4.71)		
Quorum Sensing: Yes	3.54 (2.35, 5.08)		
Difference	-0.45 (-0.99, 0.07)	0.05	
Pathogen motility: No	3.44 (1.85, 4.47)		
Pathogen motility: Yes	3.24 (2.05, 4.75)		
Difference	-0.27 (-0.72, 0.14)	0.07	
Random effects	Posterior mode (CI)	Phylo H ² (CI)	
Case fatality rate	Phylogenetic variance (V_{a1})	0.01 (0.00, 1.70)	0.08 (0.00, 28.83)
	Residual variance (V_{e1})	3.64 (2.29, 8.43)	
Generation time	Phylogenetic variance (V_{a2})	1.54 (0.95, 2.50)	99.46 (92.77, 99.98)
	Residual variance (V_{e2})	0.01 (0.001, 0.16)	
Correlation	Type of correlation	Posterior mode (CI)	pMCMC
Case fatality rate: Generation time	Phylogenetic correlation ($Cov_{a1, a2}/\sqrt{V_{a1} * V_{a2}}$)	0.99 (-0.87, 0.99)	0.26
	Residual correlation ($Cov_{e1, e2}/\sqrt{V_{e1} * V_{e2}}$)	-0.99 (-0.99, -0.02)	0.05

Table S4: The phylogenetic and residual correlations for bacterial species only between case fatality rate (% of cases that result in fatalities: binomial response, logit link function), and the number of generations per week (Poisson response, log link function) estimated using multi-response phylogenetic mixed models with life-history traits included as fixed effects. Fixed effect estimates are on the scale of the link function for each response trait.

		Posterior mode (CI)	Phylo H ² (CI)
	Ingestion vs skin	0.36 (-0.29, 1.06)	0.16
	Inhalation vs skin	0.04 (-0.75, 0.83)	0.48
	Symptoms: hinder (1)	3.37 (1.80, 4.76)	
	Symptoms: no effect (2)	3.73 (2.21, 4.63)	
	Symptoms: help (3)	3.39 (2.13, 4.38)	
	Difference 1 - 2	-0.10 (-1.19, 0.86)	0.43
	Difference 1 - 3	0.48 (-0.80, 1.10)	0.37
	Difference 2 - 3	0.27 (-0.24, 0.80)	0.17
	Facultative	3.52 (2.12, 4.86)	
	Obligate	3.31 (2.00, 4.69)	
	Difference	0.22 (-0.39, 0.80)	0.26
	Quorum Sensing: No	3.73 (2.04, 4.79)	
	Quorum Sensing: Yes	4.02 (2.53, 5.25)	
	Difference	-0.51 (-1.04, 0.06)	0.03
	Pathogen motility: No	3.43 (1.87, 4.87)	
	Pathogen motility: Yes	3.47 (2.21, 5.15)	
	Difference	-0.91 (-2.36, 1.08)	0.22
	Random effects	Posterior mode (CI)	Phylo H ² (CI)
Case fatality rate	Phylogenetic variance (V_{a1})	0.03 (0.00, 2.63)	0.13 (0.00, 35.16)
	Residual variance (V_{e1})	4.99 (2.78, 11.41)	
Generation time	Phylogenetic variance (V_{a2})	1.38 (0.76, 2.93)	99.85 (92.98, 99.98)
	Residual variance (V_{e2})	0.002 (0.00, 0.09)	
Correlation	Type of correlation	Posterior mode (CI)	pMCMC
Case fatality rate: Generation time	Phylogenetic correlation ($Cov_{a1, a2}/\sqrt{V_{a1} * V_{a2}}$)	0.99 (-0.98, 1.00)	0.38
	Residual correlation ($Cov_{e1, e2}/\sqrt{V_{e1} * V_{e2}}$)	-0.99 (-0.99, 0.64)	0.11

Table S5: The phylogenetic and residual correlations between case fatality rate (% of cases that result in fatalities: binomial response, logit link function), number of generations per week (Poisson response, log link function) and infectious dose (count of parasites: Poisson response, log link function) across human pathogens estimated using multi-response phylogenetic mixed models with life-history traits included as fixed effects. Fixed effect estimates are on the scale of the link function for each response trait.

Response Trait	Fixed effects	Posterior mode (CI)	pMCMC
Case fatality rate	Immune subversion: No Immune subversion: Yes Difference	-1.51 (-5.47, 1.79) 0.29 (-3.10, 3.69) 0.21 (-2.72, 3.29)	0.90
	Infection route: Ingestion Infection route: Inhalation Infection route: Skin Ingestion vs inhalation Ingestion vs skin Inhalation vs skin	-3.24 (-6.18, -0.45) 1.08 (-1.17, 4.98) 0.23 (-2.95, 3.07) -5.01 (-8.12, -0.90) -2.35 (-6.53, 0.13) 1.99 (-1.47, 5.10)	0.002 0.04 0.16
	Symptoms: hinder (1) Symptoms: no effect (2) Symptoms: help (3) Difference 1 vs 2 Difference 1 vs 3 Difference 2 vs 3	0.43 (-3.51, 3.53) 0.11 (-2.92, 4.10) -1.88 (-5.86, 0.76) -0.16 (-6.07, 3.19) 1.68 (-2.20, 7.15) 4.55 (-1.20, 7.06)	0.34 0.19 0.08
	Facultative Obligate Difference	-0.32 (-4.05, 3.36) -0.43 (-4.15, 2.77) -0.61 (-3.74, 2.02)	0.48
	Quorum Sensing: No Quorum Sensing: Yes Difference	0.58 (-3.28, 3.85) -2.48 (-5.25, 2.21) -2.27 (-4.62, 0.83)	0.19
	Pathogen motility: No Pathogen motility: Yes Difference	0.36 (-3.04, 4.47) 0.37 (-4.55, 2.43) -1.19 (-3.73, 2.04)	0.66
Generation Time	Immune subversion: No Immune subversion: Yes Difference	3.16 (1.79, 4.79) 3.35 (2.07, 4.65) 0.30 (-0.33, 0.74)	0.62
	Infection route: Ingestion Infection route: Inhalation	2.83 (1.54, 4.24) 2.18 (0.91, 3.67)	

Infection route: Skin	2.37 (1.17, 3.72)	
Ingestion vs inhalation	0.53 (-0.21, 1.16)	0.11
Ingestion vs skin	0.41 (-0.19, 1.01)	0.10
Inhalation vs skin	-0.06 (-0.84, 0.73)	0.45
Symptoms: hinder (1)	2.73 (1.18, 4.22)	
Symptoms: no effect (2)	3.07 (1.68, 3.97)	
Symptoms: help (3)	2.72 (1.39, 3.57)	
Difference 1 vs 2	0.03 (-1.03, 1.02)	0.45
Difference 1 vs 3	0.35 (-0.89, 1.14)	0.37
Difference 2 vs 3	0.34 (-0.26, 0.75)	0.15
Facultative	3.21 (1.38, 4.28)	
Obligate	2.60 (1.18, 4.19)	
Difference	-0.15 (-0.57, 0.49)	0.48
Quorum Sensing: No	2.68 (1.13, 4.06)	
Quorum Sensing: Yes	2.91 (1.66, 4.59)	
Difference	0.36 (-0.06, 1.03)	0.06
Pathogen motility: No	3.13 (1.28, 4.17)	
Pathogen motility: Yes	2.99 (1.76, 4.54)	
Difference	0.30 (-0.12, 0.80)	0.14
Infective dose	Immune subversion: No	4.95 (1.52, 7.68)
	Immune subversion: Yes	0.02 (-3.43, 1.93)
	Difference	-4.53 (-6.67, -1.91) <0.001
Infection route	Infection route: Ingestion	2.19 (0.14, 5.48)
	Infection route: Inhalation	0.18 (-2.65, 3.29)
	Infection route: Skin	1.77 (-1.35, 4.67)
	Ingestion vs inhalation	2.36 (-0.89, 5.85)
	Ingestion vs skin	2.18 (-1.99, 4.27)
	Inhalation vs skin	-1.50 (-4.89, 2.14)
		0.24
Symptoms	Symptoms: hinder (1)	0.62 (-2.38, 3.99)
	Symptoms: no effect (2)	2.76 (-0.94, 5.04)
	Symptoms: help (3)	2.41 (-1.09, 4.54)
	Difference 1 vs 2	-1.25 (-5.19, 2.70)
	Difference 1 vs 3	-0.11 (-4.66, 2.81)
	Difference 2 vs 3	-0.28 (-2.36, 3.38)
		0.41
Pathogen motility	Facultative	1.67 (-0.73, 4.84)
	Obligate	2.62 (-0.35, 5.38)
	Difference	1.19 (-0.69, 4.02)
Quorum Sensing	Quorum Sensing: No	0.46 (-1.84, 3.61)
	Quorum Sensing: Yes	4.04 (1.21, 6.79)

	Difference	3.38 (0.94, 5.61)	0.008
Pathogen motility: No	2.48 (-1.37, 4.13)		
Pathogen motility: Yes	2.85 (0.43, 5.98)		
Difference	2.28 (-0.37, 4.21)	0.11	
Response Traits	Type of correlation	Posterior mode (CI)	pMCMC
Case fatality rate: Generation time	Phylogenetic correlation $(Cov_{a1, a2}/\sqrt{V_{a1} * V_{a2}})$	-0.99 (-0.99, 0.98)	0.30
	Residual correlation $(Cov_{e1, e2}/\sqrt{V_{e1} * V_{e2}})$	0.13 (-0.99, 0.70)	0.37
Case fatality rate: Infective dose	Phylogenetic correlation $(Cov_{a1, a3}/\sqrt{V_{a1} * V_{a3}})$	-0.99 (-0.99, 0.98)	0.98
	Residual correlation $(Cov_{e1, e3}/\sqrt{V_{e1} * V_{e3}})$	-0.58 (-0.78, -0.23)	0.001
Generation time: Infective dose	Phylogenetic correlation $(Cov_{a2, a3}/\sqrt{V_{a2} * V_{a3}})$	0.99 (0.16, 0.99)	0.02
	Residual correlation $(Cov_{e2, e3}/\sqrt{V_{e2} * V_{e3}})$	-0.96 (-0.99, 0.80)	0.24
Response Trait	Random effects	Posterior mode (CI)	Phylo H² (CI)
Case fatality rate	Phylogenetic variance (V_{a1})	0.10 (0.000, 14.68)	0.14 (0.000, 21.58)
	Residual variance (V_{e1})	52.05 (33.29, 88.13)	
Generation time	Phylogenetic variance (V_{a2})	1.54 (0.95, 2.50)	99.50 (90.78, 99.97)
	Residual variance (V_{e2})	0.01 (0.001, 0.16)	
Infective dose	Phylogenetic variance (V_{a3})	3.48 (0.02, 28.52)	17.86 (0.10, 67.96)
	Residual variance (V_{e3})	17.66 (9.21, 33.01)	

Supplementary R code

Priors that were tested for MR-BPMMs

```
MR_Prior1 = list(R = list(V = diag(2), nu=0.002), G = list(G1=list(V = diag(2)*(0.002/1.002), nu =1.002))
```

```
MR_Prior2 = list(G=list(G1=list(V=diag(2),n=0.002,alpha.mu=rep(0,2), alpha.V=diag(2)*1000)),R=list(V=diag(2),n=0.002))
```

```
MR_Prior3 = list(R = list(V = diag(3), nu=0.002), G = list(G1=list(V = diag(3)*(0.002/2.002), nu =2.002))
```

```
MR_Prior4 = list(R=list(V=diag(3),n=0.002),G=list(G1=list(V=diag(3),n=1,alpha.mu=rep(0,3), alpha.V=diag(3)*1000)))
```

R code for Table S1

```
MCMCglmm(cbind(cbind(%_dead, %_alive), generations_week) ~ trait-1, random = ~us(trait):animal, rcov = ~us(trait):units, pedigree=tree, family =c("multinomial2","poisson"), nodes="ALL", data = data, prior=MR_Prior2, nitt=10000000, burnin=5000000, thin=5000)
```

R code for Table S2

```
MCMCglmm(cbind(cbind(%_dead, %_alive), generations_week) ~ trait-1, random = ~us(trait):animal, rcov = ~us(trait):units, pedigree=tree, family =c("multinomial2","poisson"), nodes="ALL", data = bacteria_data, prior=MR_Prior2, nitt=10000000, burnin=5000000, thin=5000)
```

R code for Table S3

```
MCMCglmm(cbind(cbind(%_dead, %_alive), generations_week, Infectious_dose) ~ trait-1 + trait:immune_subversion + trait:infection_route + trait:symptoms + trait:obligate_pathogen + trait:quorum_sensing + trait:motility, random = ~us(trait):animal, rcov = ~us(trait):units, pedigree=tree, family =c("multinomial2","poisson"), nodes="ALL", data = data, prior=MR_Prior2, nitt=10000000, burnin=5000000, thin=5000)
```

R code for Table S4

```
MCMCglmm(cbind(cbind(%_dead, %_alive), generations_week, Infectious_dose) ~ trait-1 + trait:immune_subversion + trait:infection_route + trait:symptoms + trait:obligate_pathogen + trait:quorum_sensing + trait:motility, random = ~us(trait):animal, rcov = ~us(trait):units,
```

```
pedigree=tree, family =c("multinomial2","poisson","poisson"), nodes="ALL", data = data,
prior=MR_Prior4, nitt=10000000, burnin=5000000, thin=5000)
```

Table S6: Pathogen species and life history data

Species	Obligate or facultative human parasitism	Immune subversion	Generation time (hr)	Case fatality rate (%)	QS-reg. virulence	Infection route	Effect of symptoms of infection on transmission	Motility	Infective dose	Source
<i>Acinetobacter ADP1</i>	Facultative	0	0.5	?	0	Skin	No effect	0	?	[1-4]
<i>Actinobacillus actinomycetemcomitans</i>	Facultative	1	11	25.5	0	Skin	No effect	0	?	[5-9]
<i>Aeromonas hydrophila</i>	Facultative	0	0.35	?	1	Ingestion	Helps	1	50,500,000	[10-13]
<i>Anaplasma phagocytophilum</i>	Facultative	1	21.6	1.5	0	Skin	Hinders	?	?	[1,14-16]
<i>Arcobacter butzleri</i>	Facultative	?	0.66	0.4	0	Ingestion	Helps	1	?	[1,14-17]
<i>Bacillus anthracis</i>	Facultative	1	0.5	20	1	Skin	Helps	0	20,250	[1,10,18]
<i>Bacillus cereus</i>	Facultative	0	0.3	0	1	Ingestion	Helps	1	1,000,000	[1,10,18]
<i>Bacteroides fragilis</i>	Facultative	1	0.63	19.3	0	Skin	No effect	0	?	[2,19]
<i>Bordetella</i>	Obligate	0	3.8	1	0	Inhalation	Helps	0	200	[1,20,

<i>pertussis</i>											21]
<i>Brucella abortus</i>	Facultative	1	2	1.025	1	Ingestion	No effect	0	55	[18,22-25]	
<i>Brucella melitensis</i>	Facultative	1	2	3.25	1	Ingestion	No effect	0	55	[1,10,18,22-24]	
<i>Burkholderia pseudomallei</i>	Facultative	1	1	38.5	1	Inhalation	No effect	1	10	[10,25,26]	
<i>Burkholderia mallei</i>	Facultative	1	0.75	38.5	1	Inhalation	No effect	0	10	[1,10,25,26]	
<i>Campylobacter jejuni</i>	Facultative	1	1.1	0.4	0	Ingestion	Helps	1	550	[1,10,18]	
<i>Clostridium perfringens</i>	Facultative	1	0.2	0.07	1	Ingestion	Helps	1	100,000	[1,10,18]	
<i>Coxiella burnetii</i>	Facultative	1	8	3	0	Inhalation	No effect	0	10	[1,10,18]	
<i>Cronobacter sakazakii</i>	Facultative	1	0.23	60	1	Skin	Hinders	1	1000	[1,27-29]	
<i>Cryptosporidium parvum</i>	Facultative	1	13	0.5	0	Ingestion	Helps	1	5.5	[18,30,31]	
<i>Escherichia coli</i>	Obligate	0	0.5	0.025	1	Ingestion	Helps	1	50,500,000	[10,18]	

EaggEC

<i>Escherichia coli</i>	Obligate	1	0.33	0.254	1	Ingestion	Helps	1	10	[10,18]
<i>EHEC</i>										
<i>Escherichia coli</i>	Obligate	1	0.4	0.025	0	Ingestion	Helps	1	10	[10,18]
<i>EIEC</i>										
<i>Escherichia coli</i>	Obligate	0	0.4	0.025	1	Ingestion	Helps	1	3.37E+09	[10,18]
<i>EPEC</i>										
<i>Escherichia coli</i>	Obligate	0	0.33	0.025	1	Ingestion	Helps	1	2.55E+09	[10,18]
<i>ETEC</i>										
<i>Entamoeba histolytica</i>	Facultative	1	9.6	2	1	Ingestion	Helps	1	1	[18,32, 33]
<i>Enterococcus faecalis</i>	Facultative	0	0.5	0.01	1	Ingestion	Helps	0	10,000,000	[1,10, 34]
<i>Francisella tularensis, holarkctica</i>	Facultative	1	3	0	1	Ingestion	Hinders	0	1000	[1,18]
<i>Francisella tularensis, tularensis</i>	Facultative	1	3	14	1	Inhalation	Hinders	0	7.5	[1,10, 18]
<i>Gardnerella vaginalis</i>	Facultative	0	13.5	0	1	Skin	Helps	0	2.00E+10	[10,34]

<i>Giardia lamblia</i>	Facultative	0	10.5	0.6	0	Ingestion	Helps	1	10	[18,34]
<i>Haemophilus ducreyi</i>	Obligate	1	1.8	0	0	Skin	Helps	1	30	[1,10]
<i>Helicobacter pylori</i>	Obligate	1	2.4	3	0	Ingestion	Helps	1	10,000	[1-3, 19]
<i>Histoplasma capsulatum</i>	Facultative	1	13	6	1	Inhalation	No effect	0	10	[1,18, 35-37]
<i>Legionella pneumophila</i>	Obligate	1	3.3	17.5	1	Inhalation	No effect	1	140,000	[10,18]
<i>Listeria monocytogenes</i>	Obligate	1	1	30	1	Ingestion	No effect	1	1000	[1,10, 18]
<i>Mycobacterium tuberculosis</i>	Obligate	1	19	50	0	Inhalation	Helps	0	10	[10,18, 38]
<i>Mycoplasma pneumonia</i>	Obligate	0	6	36.3	0	Inhalation	Helps	1	5,050,000	[1,10, 39]
<i>Neisseria meningitidis</i>	Obligate	0	0.72	20.3	0	Inhalation	No effect	0	1000	[1,10, 14]
<i>Neisseria gonorrhoeae</i>	Obligate	1	0.58	0	0	Skin	Hinders	0	1050	[1,10, 18]
<i>Orientia tsutsugamushi</i>	Facultative	1	9	60	0	Skin	Hinders	0	3	[10,40]

<i>Plasmodium falciparum</i>	Obligate	1	24	4	0	Skin	Helps	1	?	[41-43]
<i>Plesiomonas shigelloides</i>	Facultative	0	0.43	6	0	Ingestion	Helps	1	1,000,000	[10,44]
<i>Pseudomonas aeruginosa</i>	Facultative	0	0.5	47	1	Skin	Helps	1	1000	[1,10,18]
<i>Rickettsia conorii</i>	Obligate	1	4.1	2.1	0	Skin	Hinders	0	10	[1,18,40]
<i>Rickettsia prowazekii</i>	Obligate	1	10	30	0	Skin	Hinders	0	10	[1,10,18]
<i>Rickettsia rickettsia</i>	Obligate	1	9	65	0	Skin	Hinders	0	10	[1,10,18,45]
<i>Salmonella enterica Typhi</i>	Obligate	1	0.4	4	0	Ingestion	No effect	1	100,000	[10]
<i>Salmonella enterica</i>	Facultative	1	0.4	4	1	Ingestion	Helps	1	100,000	[1,10,18]
<i>Typhimurium</i>										
<i>Salmonella paratyphi</i>	Obligate	1	0.4	4	0	Ingestion	No effect	1	1000	[1,18]
<i>Shigella dysenteriae</i>	Obligate	1	0.67	0.6	0	Ingestion	Helps	0	10	1,46]

<i>Shigella flexneri</i>	Obligate	1	0.68	0.1	0	Ingestion	Helps	0	100	[2,18]
<i>Shigella sonnei</i>	Obligate	1	0.5	0.9	0	Ingestion	Helps	0	75	[1,47]
<i>Staphylococcus aureus</i>	Facultative	1	0.4	4	1	Ingestion	No effect	0	100,000	[1,10,18]
<i>Stenotrophomonas maltophilia</i>	Obligate	0	0.6	?	1	Ingestion	No effect	1	5.01E+08	[1,10]
<i>pneumoniae</i>										
<i>Streptococcus pyogenes</i>	Obligate	1	0.4	19	1	Inhalation	No effect	0	1000	[1,10,18]
<i>Treponema pallidum</i>	Obligate	1	33	3.17	0	Skin	Helps	1	57	[1,10,48]
<i>Vibrio cholera</i>	Obligate	0	0.2	0.9	1	Ingestion	Helps	1	3.33E+10	[1,10,18,34]
<i>Vibrio parahaemolyticus</i>	Facultative	0	0.2	0.01	1	Ingestion	No effect	1	55,000,000	[1,10,34]
<i>Vibrio vulnificus</i>	Facultative	1	0.16	39	1	Ingestion	Helps	1	100	[1,10,34]
<i>Yersinia enterocolitica</i>	Facultative	1	0.55	0.5	1	Ingestion	Helps	1	1,000,000	[10,18]
<i>Yersinia pseudotuberculosis</i>	Facultative	1	0.5	0.5	1	Ingestion	No effect	0	1,000,000	[1,10,34]

<i>Yersinia pestis</i>	Facultative	1	1.25	90	1	Skin	Helps	0	10	[1,10, 18]
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